

### **AMENDMENTS TO THE CLAIMS**

1. (Previously Presented) A method comprising:
  - a) placing a plurality of labeled proteins, polypeptides or peptides in a plurality of chambers, such that different chambers contain a different type of labeled amino acid;
  - b) passing the labeled proteins, polypeptides or peptides through one or more nanopores, an inner surface of the nanopores coated with a semiconductor material;
  - c) detecting labeled amino acid residues in the labeled proteins, polypeptides or peptides;
  - d) compiling an amino acid distance map for each type of labeled amino acid; and
  - e) identifying the protein based on the distance maps.
  
2. (Previously presented) The method of claim 1, further comprising:
  - a) placing a template nucleic acid into each chamber; and
  - b) producing one or more labeled proteins, polypeptides or peptides encoded by the template nucleic acid.
  
3. (Original) The method of claim 1, further comprising: a) obtaining one or more proteins, polypeptides or peptides from a biological sample; and b) labeling the proteins, polypeptides or peptides post-translationally.

4. (Original) The method of claim 1, wherein the protein, polypeptide or peptide is identified by comparing the distance maps with a library of amino acid distance maps.
5. (Original) The method of claim 1, wherein the protein, polypeptide or peptide is identified by comparing the distance maps with the sequences of known proteins.
6. (Original) The method of claim 2, wherein each chamber is operably coupled to a different set of nanopores.
7. (Original) The method of claim 1, wherein each nanopore is operably coupled to a detector.
8. (Original) The method of claim 1, wherein only one labeled protein, polypeptide or peptide passes through a nanopore at a time.
9. (Canceled)
10. (Original) The method of claim 1, wherein the length of time between passage of a first labeled amino acid through the nanopore and passage of a second labeled amino acid through the nanopore corresponds to the distance along the labeled protein, polypeptide or peptide between the first and second amino acids.

11. (Original) The method of claim 1, wherein the labels are selected from the group consisting of luminescent labels, fluorescent labels, phosphorescent labels, chemiluminescent labels, conductive labels, nuclear magnetic resonance labels, mass spectroscopy labels, electron spin resonance labels, electron paramagnetic resonance labels and Raman labels.

12. (Original) The method of claim 1, wherein at least one end of the labeled protein, polypeptide or peptide is attached to an identifiable label.

13. (Original) The method of claim 1, wherein said labeled amino acids are detected with a photodetector.

14. (Original) The method of claim 1, wherein said labeled amino acids are detected with an electrical detector.

15. (Original) The method of claim 2, further comprising analyzing a multiplicity of labeled proteins, polypeptides or peptides from each chamber.

16. (Original) The method of claim 1, further comprising determining at least a partial sequence of the protein, polypeptide or peptide based on the distance maps.

17-31. (Canceled)

32. (New) The method of claim 2, wherein the one or more labeled proteins, polypeptides or peptides encoded by the template nucleic acid is produced by *in vitro* translation or by linked transcription/translation.

33. (New) The method of claim 32, wherein *in vitro* translation is performed with mRNA templates.

34. (New) The method of claim 32, wherein *in vitro* translation is based on rabbit reticulocyte lysates, wheat germ extracts, or *E. coli* extracts

35. (New) The method of claim 1, wherein the distance map shows distances in a sub-nanometer scale.